

COMPARING METABOLOMIC PROFILES OF ASIAN AND NORTH AMERICAN ASH SPECIES (GENUS *FRAXINUS*) TO INVESTIGATE THE BASIS FOR RESISTANCE TO EMERALD ASH BORER

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At present, North American ash (*Fraxinus* spp.) are under attack by the emerald ash borer (*Agrilus planipennis* Fairmaire; EAB), an invasive species native to eastern Asia. Interestingly, Asian ash species are comparatively resistant to this phloem-feeding insect. Most researchers currently working on EAB are focused on improving detection, monitoring, biological control, and eradication methods in an attempt to protect our population of North American ashes against the advancing infestation front. To date, however, little work has been done to determine why our North American ash species seem to be so markedly different from the Asian ash species in EAB susceptibility. If we can determine that the difference is due to metabolites produced by one species but not by another, we might be able to exploit those differences to engineer ash trees with elevated resistance to EAB. One objective of this research is to compare the metabolomic profiles of North American and Asian ash species. Seedlings of susceptible

North American ash species (white, green, black) are being grown in a greenhouse alongside resistant Asian ash species (Chinese, Manchurian), plus two European ash species that have unknown resistance. Seedlings will be challenged with methyl jasmonate root drenches to simulate insect feeding; some will be left untreated to serve as controls. Phloem, root, and leaf samples will be harvested from each seedling at various times and subjected to high performance liquid chromatography-mass spectrometry and gas chromatography-mass spectrometry analyses. Additionally, high-throughput sequencing is being used to compare the transcriptomic profiles of infested and uninfested green ash trees in an attempt to determine genes that are up- or down-regulated in response to EAB feeding. Once candidate genes have been identified, a set of molecular experiments will be conducted to investigate the function of various genes in the jasmonate pathway in tissue harvested from these same trees.